

SEQUENCE LISTING

(1) GENERAL INFORMATION:

(i) APPLICANT: Genentech, Inc.
Schwall, Ralph H.
Tabor, Kelly Helen

(ii) TITLE OF INVENTION: Hepatocyte Growth Factor Receptor
Antagonists and Uses Thereof

(iii) NUMBER OF SEQUENCES: 4

(iv) CORRESPONDENCE ADDRESS:

(A) ADDRESSEE: Genentech, Inc.
(B) STREET: 460 Point San Bruno Blvd
(C) CITY: South San Francisco
(D) STATE: California
(E) COUNTRY: USA
(F) ZIP: 94080

(v) COMPUTER READABLE FORM:

(A) MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
(B) COMPUTER: IBM PC compatible
(C) OPERATING SYSTEM: PC-DOS/MS-DOS
(D) SOFTWARE: WinPatin (Genentech)

(vi) CURRENT APPLICATION DATA:

(A) APPLICATION NUMBER:
(B) FILING DATE:
(C) CLASSIFICATION:

(vii) PRIOR APPLICATION DATA:

(A) APPLICATION NUMBER: 08/460368
(B) FILING DATE: 02-JUN-1995

(viii) ATTORNEY/AGENT INFORMATION:

(A) NAME: Marschang, Diane L.
(B) REGISTRATION NUMBER: 35,600
(C) REFERENCE/DOCKET NUMBER: P0938P1PCT

(ix) TELECOMMUNICATION INFORMATION:

(A) TELEPHONE: 415/225-5416
(B) TELEFAX: 415/952-9881
(C) TELEX: 910/371-7168

(2) INFORMATION FOR SEQ ID NO:1:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 220 amino acids
(B) TYPE: Amino Acid
(D) TOPOLOGY: Linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

Asp Ile Met Met Ser Gln Ser Pro Ser Ser Leu Thr Val Ser Val
1 5 10 15

Gly Glu Lys Val Thr Val Ser Cys Lys Ser Ser Gln Ser Leu Leu
 20 25 30
 Tyr Thr Ser Ser Gln Lys Asn Tyr Leu Ala Trp Tyr Gln Gln Lys
 35 40 45
 5 Pro Gly Gln Ser Pro Lys Leu Leu Ile Tyr Trp Ala Ser Thr Arg
 50 55 60
 Glu Ser Gly Val Pro Asp Arg Phe Thr Gly Ser Gly Ser Gly Thr
 65 70 75
 10 Asp Phe Thr Leu Thr Ile Thr Ser Val Lys Ala Asp Asp Leu Ala
 80 85 90
 Val Tyr Tyr Cys Gln Gln Tyr Tyr Ala Tyr Pro Trp Thr Phe Gly
 95 100 105
 Gly Gly Thr Lys Leu Glu Ile Lys Arg Thr Val Ala Ala Pro Ser
 110 115 120
 15 Val Phe Ile Phe Pro Pro Ser Asp Glu Gln Leu Lys Ser Gly Thr
 125 130 135
 Ala Ser Val Val Cys Leu Leu Asn Asn Phe Tyr Pro Arg Glu Ala
 140 145 150
 20 Lys Val Gln Trp Lys Val Asp Asn Ala Leu Gln Ser Gly Asn Ser
 155 160 165
 Gln Glu Ser Val Thr Glu Gln Asp Ser Lys Asp Ser Thr Tyr Ser
 170 175 180
 Leu Ser Ser Thr Leu Thr Leu Ser Lys Ala Asp Tyr Glu Lys His
 185 190 195
 25 Lys Val Tyr Ala Cys Glu Val Thr His Gln Gly Leu Ser Ser Pro
 200 205 210
 Val Thr Lys Ser Phe Asn Arg Gly Glu Cys
 215 220

(2) INFORMATION FOR SEQ ID NO:2:

- 30 (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 230 amino acids
 - (B) TYPE: Amino Acid
 - (D) TOPOLOGY: Linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

35 Glx Val Gln Leu Gln Gln Ser Gly Pro Glu Leu Val Arg Pro Gly
 1 5 10 15
 Ala Ser Val Lys Met Ser Cys Arg Ala Ser Gly Tyr Thr Phe Thr
 20 25 30
 Ser Tyr Trp Leu His Trp Val Lys Gln Arg Pro Gly Pro Gly Leu

	35	40	45
	Glu Trp Ile Gly Met Ile Asp Pro Ser Asn Ser Asp Thr Arg Phe		
	50	55	60
5	Asn Pro Asn Phe Lys Asp Lys Ala Thr Leu Asn Val Asp Arg Ser		
	65	70	75
	Ser Asn Thr Ala Tyr Met Leu Leu Ser Ser Leu Thr Ser Ala Asp		
	80	85	90
	Ser Ala Val Tyr Tyr Cys Ala Thr Tyr Gly Ser Tyr Val Ser Pro		
	95	100	105
10	Leu Asp Tyr Trp Gly Gln Gly Thr Ser Val Thr Val Ser Ser Ala		
	110	115	120
	Ser Thr Lys Gly Pro Ser Val Phe Pro Leu Ala Pro Ser Ser Lys		
	125	130	135
15	Ser Thr Ser Gly Gly Thr Ala Ala Leu Gly Cys Leu Val Lys Asp		
	140	145	150
	Tyr Phe Pro Glu Pro Val Thr Val Ser Trp Asn Ser Gly Ala Leu		
	155	160	165
	Thr Ser Gly Val His Thr Phe Pro Ala Val Leu Gln Ser Ser Gly		
	170	175	180
20	Leu Tyr Ser Leu Ser Ser Val Val Thr Val Pro Ser Ser Ser Leu		
	185	190	195
	Gly Thr Gln Thr Tyr Ile Cys Asn Val Asn His Lys Pro Ser Asn		
	200	205	210
25	Thr Lys Val Asp Lys Lys Val Glu Pro Lys Ser Cys Asp Lys Thr		
	215	220	225
	His Thr Ala Ala Pro		
	230		

(2) INFORMATION FOR SEQ ID NO:3:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 660 base pairs
- (B) TYPE: Nucleic Acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

35 GACATTATGA TGTCCCAGTC TCCATCCTCC CTAAGTGTGT CAGTTGGAGA 50

GAAGGTTACT GTGAGCTGCA AGTCCAGTCA GTCCCTTTTA TATACTAGCA 100

GTCAGAAGAA CTAAGTGGCC TGGTACCAGC AGAAACCAGG TCAGTCTCCT 150

AAACTGCTGA TTTACTGGGC ATCCACTAGG GAATCTGGGG TCCCTGATCG 200
CTTCACAGGC AGTGGATCTG GGACAGATTT CACTCTCACC ATCACCAGTG 250
TGAAGGCTGA CGACCTGGCA GTTTATTACT GTCAGCAATA TTATGCCTAT 300
CCGTGGACGT TCGGTGGAGG CACAAAGTTG GAGATCAAAC GGACCGTGGC 350
5 TGCACCATCT GTCTTCATCT TCCCGCCATC TGATGAGCAG TTGAAATCTG 400
GAACTGCCTC TGTGTGTGTC CTGCTGAATA ACTTCTATCC CAGAGAGGCC 450
AAAGTACAGT GGAAGGTGGA TAACGCCCTC CAATCGGGTA ACTCCAGGA 500
GAGTGTACA GAGCAGGACA GCAAGGACAG CACCTACAGC CTCAGCAGCA 550
CCCTGACGCT GAGCAAAGCA GACTACGAGA AACACAAAGT CTACGCCTGC 600
10 GAAGTCACCC ATCAGGGCCT GAGCTCGCCC GTCACAAAGA GCTTCAACAG 650
GGGAGAGTGT 660

(2) INFORMATION FOR SEQ ID NO:4:

(i) SEQUENCE CHARACTERISTICS:

- 15 (A) LENGTH: 690 base pairs
(B) TYPE: Nucleic Acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

SAGGTTCAGC TGCAGCAGTC TGGGCCTGAA CTGGTGAGGC CTGGGGCTTC 50
20 AGTGAAAATG TCCTGCAGGG CTTCGGGCTA TACCTTCACC AGCTACTGGT 100
TGCACTGGGT TAAACAGAGG CCTGGACCAG GCCTTGAGTG GATTGGCATG 150
ATTGATCCTT CCAATAGTGA CACTAGGTTT AATCCGAACT TCAAGGACAA 200
GGCCACATTG AATGTAGACA GATCTTCCAA CACAGCCTAC ATGCTGCTCA 250
GCAGCCTGAC ATCTGCTGAC TCTGCAGTCT ATTACTGTGC CACATATGGT 300
25 AGCTACGTTT CCCCTCTGGA CTACTGGGGT CAAGGAACCT CAGTCACCGT 350
CTCTTCCGCC TCCACCAAGG GCCCATCGGT CTTCCCCCTG GCACCCTCCT 400
CCAAGAGCAC CTCTGGGGGC ACAGCGGCCC TGGGCTGCCT GGTCAAGGAC 450
TACTTCCCCG AACCGGTGAC GGTGTCGTGG AACTCAGGCG CCCTGACCAG 500
CGGCGTGAC ACCTTCCCGG CTGTCCTACA GTCCTCAGGA CTCTACTCCC 550
30 TCAGCAGCGT GGTGACCGTG CCCTCCAGCA GCTTGGGCAC CCAGACCTAC 600
ATCTGCAACG TGAATCACAA GCCCAGCAAC ACCAAGGTCG ACAAGAAAGT 650

WO 96/38557

PCT/US96/08094

TGAGCCCAAA TCTTGTGACA AAATCACAC AGCTGCGCCG 690